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; Sequence 12, Application US/10030203
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; TITLE OF INVENTION: Neovascular-Targeted Immunoconjugates
; FILE REFERENCE: OCR-679B, US
; CURRENT APPLICATION NUMBER: US/10/030, 203
; PRIORITY FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/US00/16481
; PRIORITY FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: MS DOS
; SEQ ID NO 12
; LENGTH: 2138
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: hfv1aam immunoconjugate
; OTHER INFORMATION: includes leader + hfv1aam + human IgG1Fc
US-10-030-203-12.1
KLEGRDFIMVGOALRLGLLGLQCLAGVAKASGGETRDMPKPGFHRVFTVQEBAGVLRHRRANA
FLEELRLEJMECEKCEQCFEERBEIFKDAERTKLPWISYSDGDCSPCCNGSCDKDLOSITCPCL
PAFEGNCEHNDOLLI CVENNGGCEQYCSHDGTGKSCRCHEGSLADGVSCTPYEFGKPILEK
RNASKRQGRIVGGVCPKSGCPHVOVLLVNGAOLCGGLINTIIVVSAHGPDKIKMNRNLIIVLGEHDL
SEHDGBQSRVAVOVIIPSTYVPGTTHDIALRLHQPVTIDHVPILCLBERTBERTTLAFAVRSLVSG
WGQLDRGATVLEMTAVNPLMTQDCLQOSRKVDSNPITVYMCAGYSDGSDSCAGSGGPAATHYR
GTWYLTGIVMGQCAVGHGVTVTRVSOYLEMLQKLMRSEPRGVLLRAPPGSAEPKSCDKTHTCPPC
PAVELLGGFPVLEPPPKEDTLMSTRPEVTVVVDVSDHDPVFNMYVDGVEYHAKTKEPREEQVNT
YRVAVSLTVLHOMLNKKEYKCTKSNALPAPIEIKTISKAGOPREXOVTLTPSRDELTKNOVSLTCLV
KGPYEDIDAVENMSGNPENNYKTTTPVLDSDSFLYLSKLTVDKSRWQGNVSCSVMHALLNHTYQK
SLSLSPGKXXAAI
US-10-030-203-12.2
SFABISMSRPSGSSSAFCGFRAMTLOAGSLRPOEBKHGTCRGRSGLTSSXPRRKPTAECTGAGAPTR
SWRSCTBARPMRGARBSASDBRRBSRTBRGSCGGLVTMTGTVPOVAVABGAPARTSSPSASAS
LPSRAGTTRTMTSAXVTRTAAYSTAYTTRAPAPVGAITRGTLCQTCGCPAHPOULITHYEKILPYKK
EMPANPVAELMGANCAKSGVHGSRSCXMEELSCVGGXSTPSCMSRPVTVSTKSRGTIXSRCAVSTTS
ASTTGMSRAGMWRSSSPARTSRAPPTTTSRCACTSPWSLITWPCSPACNRSGLRGMWPSCASHSMA
GASCTWVAPRPMWSMCGTFCPOXSRPTACSSHGRETPOISRTCSVPATMAARTPAGTVEAHMPTTG
ARGTWRASAGARAOPMATIGCTGSPSTSGCKSCASOAHOBSSCEPHFPPQSPNLVTKLTHAHRA
OHTNSMGDRSSSPONPRTPTSPXSGRLSHAMWMTXATKLRSSTGTWTAMRCIPIROSGRSSTTAR
TWSASAPSCCTRTXMAHRSISARPTPSOPSPSKRPSKPKGSPBNKCTCPHPGMSXPTTRSAKPMS
KASIPATSPWSGRMSGRITTRRLPCWPTATPASTSSPSPWTRAGSGRTSSHAPXCMRLCTTTNRK
ASPCLRYNDKRPI
US-10-030-203-12.3
ALORFTHHGLGCPQAPLSENAASGLPCGRGRGXGLRRRTGHAVERAGASQSLRNPGRGPRRPAAPORV
PGLGAAGLPGEGVGGVAVLIRGGEDVQGRGEDEVLDLQXMGVCLSKMPBNGLDGPAVLYLILPP
CLRGPELIXDQGXVADICERRRLXAVLQXPHQALLSVPRGVLASGRGVLTTHSXISMKNYTSRKK
KCOOTPRPNCGGQVQPORGVSMAGPVVGVMSVVWGPDPQHHLGRLPFRONDELEBPRGAGRAPQ
RARGXAEPAAGAGHHPHVTAPGHHPRHRAAPAPAGPHXPCGAPARTDVLXBDAGLALLIGORL
GPAAGPMRHGPGAHGAROAPADDPGLPAVTEAGRLPKYGHVHLCRLIGMOOGLRGOWRPTCHPLPG
HVPYDGRROI.GRGLRANGPLMGVYCGLPYHVAEAKALHATAPSPSPASPISTIRBAOILIONSHMPTVP
STYTPGCTVSLPLPRTKOGHPHDLPRDXGHRGGRERPRPXGOVQVYRGRGAXCODXAGGAVOQHV
PCQGRPHRAPGLAEWGGVOVQIQOSPPSPHRNHLQSORAPRTTGVHAPAPIPGXADQSPQPDLPQO
RLLSORRRRGVGEWMAEQBOLQDHASBAGRLRLPLQOAHRGQBOVAAGERLMLRDAXGSAQPLHAE
PLPVSXGMIISGI
US-10-030-203-12.4
AAAYHLRDEBERLFCVWMLCRASCITEHEKTPPCCHLLSTVSLXKRKEPSESGTGVVTLXLSGCPLL
SHSTANSLGAKPLTROVALTMPLVSSSDGGRVYTCXSRGCPLELVPSMGAGALLLETJLHLSLPPSO
SMCRVTALITRIVYLXCSGKGLVACTSTPTVQLNLITSGSMLTSTTHVTSGVREIMRVSJGFGX
RKTDPGRRSSGAGGIGHVXVLSQDLGADPNAGARARTPRGRSEMSFCSHSMWELVLYTPKMPVAPQ
WPOLTMVRYHVPRXVAVACGPLSAPAOSSLPSXPAQNMVSVIIGESPTFRDCROSVWISRGTLSTMS
SRVAPRSSSMPOBLTWIEKRTKAVLSENVSSRGROGTMTVITGTCGRSSAMKLVVPGTVUIGMWT
ATRLGSPSCSLASGSPSTIRLOPLILSKONAAETTMQVILRVPPHAXAPPTNARTCHGHSPLGHTL
PTTIRPWLGLAFELSRIGIFPHGYSITVGVOUDTPSASRYPSMHQERLVVPVMSLOYCSQPPSPFTQISW
SLCVSQRPSPKAGROKQIXDMSVLSQBPFMHGLFAHWSPSLHIONFVLSASLXISRASKEHCSLH
SLRBPSSSRNALARRRCRTPMASSVTKTLXGPFHGMRSVSPREALATPPAQAQX6SPSRQSL
RAWETMWSLQSI
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RPLIYETPGSSAGSCGABPHASRBRBRSPAATSCPRXACCRRGRBRBRSPAREBWSGSPAHNS
PTPRCRHDSILXGRSGXGSGNSAHGMAAGCTPVYGLAALIMRFRFSWGLGGLCMRPTCTPCBSAS
PGAGRGRXPHGTCCCTAPPAUSWXYAPRRPRTSTXPOGLGSRPPPRMXPQSGRSGVLCVIGR
GRLTPPGVOVLGTVGMCCECHKIMALIRIEMGLAGLLGVLSAXAPAAITRGTGRMCTPQSGPRLRSP
GSRXCSGTCPCSGMHWGLHCPRRSPCCSPSRHRTCTPYLGLSLPSTVTAAGSGSAGARAXAPXA
PGMRHGPAPAGSRXPMRSARBPASGORTSVRAGRGA PHGXOPRAGAGARCGMWCORCTCMGXPA
PAGSAPPRABXGRABAPRSGSSSXPCRNAGPRAPPRMCKSGSPHTBLISPTTGPAMDPTPLMGTPC
POTGLGCMHFFPLEVLEFFPHMDIQLVCTTPRLPASTTRGTDRAKWCCTCGHSTHRSRBRBAGH
PCASHSGPRRQGRSYRRGAGCRSPHSGMDIRHTGPRHCKSRPAASSPRXSPGPRRSTAPCT
PSPSPAPAPGRTMRAGAGRGLPPGLRLCEBAPASTACPVTLLRXPRLQSGSPBAQLEGXAX
GPGRPXXNLCAI
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6

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US-10-030-203-12.5
GRLSPTTRQGBALLRVTVVOSLHMHGAXEDVPLIPALVHGBLAVEEGAVGVQHGRCGLVTVLRPLAL
PLHGDVAGIEAFVDAQGQADVLGQLTIGWQGVHLKFSGLPFGGDFLJGWSGFGVGDLLVLAITOPV
LVQGBDADHTVRAVVLRLCLGXMHIAVHVPELDLRVVAHVHHAACDLRGGDHGVLPWGE
EDXRSPOEFRCMAMACVSVTEFGLCGSGKMSQEDSMMLXAHBLLQPLDVGDPGVHPRKVAHGAAL
APADAROVPRAPVVGMMASIVPRAGVLAIRVAGTEHVLIDIGVSHLPXLLOAVLGHQPGHVEHBL
OGRGATVQOLAPADDOXBHAGHGRPLABRPGOARGHMVSDHGLVQASORDDVVGAGADVRAGDDDLR
HPRALLPVYLAERVYLAQHNDQVPPVLDPEVTGGRGHPGNDGPPPTOLSSITHQOODLPWTLPRGALH
PHNSALFAGISFEXNRIFSTWIFNGCAGHPVCOQVRVLPVAFGALGARVTVHVLTAALVHTTDLVI
LVRLTVLALSGREXEMADIQLSELVLAGAPILAMTXGTLVPIVTRNPEQLRLRVLEDLPLGLEGLLLAL
PLQGARPOLQOERYGABAPVQDVAVGFLGYEDSVPRPLPHRVPCFSSXGLSDPACSOALPKPKQABEP
GLADHDEISAKI
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> O <
O| 10 IntellGenetics
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FASTDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-617-619-7.res made by jdelaval on Tue 15 Feb 105 11:34:06 PST.

Query sequence being compared: US-10-617-619-7 (1-232)
Number of sequences searched: 6
Number of scores above cutoff: 6

Results of the initial comparison of US-10-617-619-7 (1-232) with:
File : trans.pep

100-
N -
U 50-
M -
B -
R -
O 10-
S -
E 5-+
C -
N -
U -
U -
C -
S -
S 0
SCORE 0 26 51 77 102 128 153 179 204 230
STDEV 1 2

PARAMETERS

Similarity matrix Unitary 1 K-tuple 2
Mismatch penalty 1.00 Joining penalty 20
Gap penalty 0.05 Window size 32
Gap size penalty 0
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean 43 Median 6 Standard Deviation 91.61
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 4270
Number of sequences searched: 6
Number of scores above cutoff: 6

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Score	Seq. Frame
1. US-10-030-203-12	Sequence 12, Application US/10030203	712	230	230	2.04 0
2. US-10-030-203-12	Sequence 12, Application US/10030203	711	7	34	-0.39 0
3. US-10-030-203-12	Sequence 12, Application US/10030203	712	6	32	-0.40 0
4. US-10-030-203-12	Sequence 12, Application US/10030203	711	5	7	-0.41 0
5. US-10-030-203-12	Sequence 12, Application US/10030203	712	5	37	-0.41 0
6. US-10-030-203-12	Sequence 12, Application US/10030203	712	5	40	-0.41 0

1. US-10-617-619-7 (1-232)

US-10-030-203-12 Sequence 12, Application US/10030203

Sequence 12, Application US/10030203
GENERAL INFORMATION:

APPLICANT: Alan Garen
APPLICANT: Zhiwei Hu
TITLE OF INVENTION: Neovascular-Targeted Immunoconjugates
FILE REFERENCE: OCR-6798 US
CURRENT APPLICATION NUMBER: US/10/030,203
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: PCT/US00/16481
PRIOR FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: MS DOS
SEQ ID NO 12
LENGTH: 2138

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

NAME/KEY: CDS
OTHER INFORMATION: hVt1asm immunoconjugate
OTHER INFORMATION: includes leader + hVt1asm + human IgG1Fc

Initial Score = 230 Optimized Score = 230 Significance = 2.04
Residue Identity = 99% Matches = 230 Mismatches = 2
Gaps = 0 Conservative Substitutions = 0

KLGRDPIVNSQALRLCLLLGLGCLAAAGVAKASGGETRDMPKRGHRVVTQBEAHGVLLHRRRAAFPL
10 20 30 40 50 60 70
BELRPSGLRECKEKGQCFEERARLFFKDAERTKLPWISYSDGDDQCASSPCQNGSKCKDQAGYICFCLPAFE
80 90 100 110 120 130 140
GRNCETHKDDOLICVNNENGGEQYCSHTGTGRSCRGEGYSLADGVSCPTVEYPCGKIPILERKNAKSP
150 160 170 180 190 200 210
QGRIVGKVCPRKGECPWQVLLVNGAQLCGGTLINTIWNVSAHCFDKIKWRNLI AVLGBHDLSEHDDQ
220 230 240 250 260 270 280
SRRAVQVLIIPSTYVPGTNHDIALLRLHQPVLTDHVVPLCLPERTSERTIAFYRPSIVSGMGLLDRCAT
290 300 310 320 330 340 350
ALELWVAVPRLMTQDDCQGRKRVGSDSPNITEYMFCAGYSDGSKDSCAGDSGPHATYRGTWLTLGISWSG
370 380 390 400 410 420 430
OGCATVGHGVTYRVSOYIEMQLKMRSEBRPGVLLRAPFOSAPKPCDKNHTCPCPAPFLIGSPVFLF
440 450 460 470 480 490 500
30 40 50 60 70 80 90 100
PPKFDOTLMISRTPEVTCVVDVSHEDBEVFNWYDGVENATKREBEQYNSYRVVSLVTLHODWLN
PPKFDOTLMISRTPEVTCVVDVSHEDBEVFNWYDGVENATKREBEQYNSYRVVSLVTLHODWLN
510 520 530 540 550 560 570
GKEYKCVSNKALPAPRIETISKAKGQPREPOVYTLPPSRDELITKNQVSLTCLVKGFGYPSDIAVENESNGOP
110 120 130 140 150 160 170

220 230 X

LNHNTOKSLSLSPGK
 AAEEDVPLPRLVHGLAVEEAGVGVGGRGLVVLRLPLPLHGDVAGIEAPDQAGADLVLGQLIPG
 30 40 X 50 60 70 80 90
 WGGVHLKFSGLPFGGDFLDGMBGVGDALVLLAIQPLVVDGEDADHTVRAVLLRLCLGKXNHLH
 100 110 120 130 140 150 160 170
 AVHVEVDLRFVAVHHAACDLRGPDHEVVLGFMBGEEDXRSPOEFRCARWACVSVFTRFGLCSGSKW
 180 190 200 210 220 230 240
 GSQESNMALXHELLOPLDVLGDPGVHPRKVAHGCALLAPADARQVPRAPVVGCMASVTRAGVLAIRV
 250 260 270 280 290 300 310
 AGTEHVLIDIMGVSHLPXLLQAVLGHQFPGHVEHLOGRATVQOLAPADQXEAHEGQPLRERPFQAGS
 320 330 340 350 360 370 380
 HMMVSEBDHGLVQAEQDDVVGARDVVRAGDDDLRHPALLIPVLAELVLAQHRDQVPEVLDLVETVGRGDH
 390 400 410 420 430 440 450
 PDGVVQGPPTQLSIHQOQDLPTLPLFGAHLAPHNSALGFAGISFFXNRYFSTWIFNCGCAGHPVQQRVPL
 460 470 480 490 500 510 520 530
 VAPRGALGARVTVAVLLTAVALVHTDQVILVLTVPALGEBADIGLEVLGAPILANTKTGLVEITV
 540 550 560 570 580 590 600
 RNPEQRLPRLVLEDLPGLEBALLLALPLQAGAPQLQERVGAPAPVQDVGILGYEDSVRPLRPHVPC
 610 620 630 640 650 660 670
 FSSKGLSDPACSOALKPKQKAEPEGLDDEISAK
 680 690 700 710

5. US-10-617-619-7 (1-232)
 US-10-030-203-12

Initial Score = 5 Optimized Score = 37 Significance = -0.41
 Residue Identity = 194 Matches = 54 Mismatches = 146
 Gaps = 71 Conservative Substitutions = 0

RPLIITYETGQSSASCSGCAEPHASRSMRRSPATSCPPRAXCCGRSRRSPAREAMSCSGSPAHMSPT
 10 20 30 40 50 60 70
 PRRCMDRSIXGDRSGXPGSMGSAHPQMGAGCTPVVLGALMLMRWPSRWGLGSLCWRPCTCTPGHSASAGAG
 80 90 100 110 120 130 140
 RXGRXPNGTCCCTAPRALSMXYADPRRRTSTXTPQGLRSGRPPPRMXPGSGRSXGCPWVLGGRLTVP
 150 160 170 180 190 200 210
 PGVOVLGTVMGCEFGCHKIWAIRIREMGLAGLLGVALSAXAPATRCTGRPMCTPGSPRLSPGSSXKCPSS
 220 230 240 250 260 270 280
 GTTCGSMHNVGLHCPRRSPCHPSRRHTCTPYXLSLPPSVTAAGSPGSSAGAXAPXAPGPRMRGPA
 290 300 310 320 330 340 350 360
 GPSRXPMSSARRPSSORTSVAGAGAPHGQXGPRAAGAACRCGMWCPGRTCMGXHAPAPAGSAHPRAR
 370 380 390 400 410 420 430
 XGRAPAPRSGSSSSXFCGNSGPRRPRRWKXGSPHTTEHLSPTTGPAADTILMKTGCPGPGGLGCMWTFP
 440 450 460 470 480 490 500
 30 40 50 60 70 80 90
 ---PPKEDTLMIKTRP---EYTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKRPREQVNSTYRVVLT
 LEVYFPHNDIQMWRTPLRLPASTPRTGTRDSAMCP-----CHCHSTASR-----RSRSHRS
 510 520 530 540 550
 100 110 120 130 140
 VLN--QDWLNGKEYKCKVNS--NKAALP--AP-----IEKTIISKAKGQFPREPQVYTLPPSR---DE

AGHP-CASHSSGPRQSGRSRYRTGAGPCRSBHSMDLHHTGPHCKSKRTYSSSR-EPXSRGPRRSTAPP
 560 570 580 590 600 610 620
 LTKNAVSLTCLVKGTFYPPDDIAVEMSNQP-----ENNYKTTPEVLDSDSGFFLYSKLTVDSKSNWQGNV
 150 160 170 180 190 200
 CTPSBGSAAAPPGTRMWDAGAGRGLPGLRLCEAPASTACPV-----FL--LIRPYRPLQPSPE
 630 640 650 660 670 680 690
 210 220 230
 SCSTVHEALHNTYOKSLSLSPGK
 AQAEGRGAAXGPGRPXNLCKA
 700 710 X

6. US-10-617-619-7 (1-232)
 US-10-030-203-12

Initial Score = 5 Optimized Score = 40 Significance = -0.41
 Residue Identity = 214 Matches = 57 Mismatches = 145
 Gaps = 68 Conservative Substitutions = 0

AAAYALPDREBLFCVXWLCRASCTIHEKTFPCCHLLISTVSLIXRKEBSESSGGLVXILFSGCPULLSH
 10 20 30 40 50 60 70
 STMSLXKXPLTROVRLTFVYSSRDGRVYTCRSRCPLALEWFSMGARALLETLHLXSLPFSQWCR
 80 90 100 110 120 130 140
 TVRLTTRTVVLYCSSRGFVLAICTSTSTYQLNLTSGSMWLTSTTHTVTSGRREIMVSLGFGKRTKTDGP
 150 160 170 180 190 200 210
 PRSSGAGHGXYVLSQDLGSDPDNGARRRTPGSGSRMFCISMWTWENTLYTPKXPTVAQPPHQLTMPV
 220 230 240 250 260 270 280
 RYHVRKXWVACGPPPLSPAOESILPSEXPQOMYSVIFGESPTFRDCRQSWVIRGTLSTWSSRAVAPRSS
 290 300 310 320 330 340 350 360

X
 EPKSCDKTHTCP-----PCPAPELLGSPSVF

WPOPLNEKRTKASVLSENVRSGRQGTWGSVRTTGMCRSSASMSWLVPGTYVLMNTCATRLRCSPPCS
 370 380 390 400 410 420 430
 LFPKRP-----KDTLMIS--RTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHN--AKTKPREEOYNS-----
 440 450 460 470 480
 LRSCSPSTAIRPLQFLILSKQMAETTMV-----LIRVPPHNAKAPFTNNRRTCHGHSPLGHT

---TYRVVSVTLVLIHQDMLNKEYKCKVSNALPAPLIEKTSKAKGQREPOVYTL-PPSRBELTKQVSLT
 490 500 510 520 530 540 550 560
 LEPTRIPWGLAFLPSRIGIPPHGVSTVGVODTPSASREYVS-WHQERLIVPVMSLQCSQPPSFTQISWS

CL-VKGFYPS-----DIAVWESNGDP---ENNYKTTTPVYL-DSGSGFFLYSKLTVVKSRRQGNVSCSV
 570 580 590 600 610 620 630
 SLCSVQFPPPSAKGRKOIXDMSWSLQEBPFMHGLEAHMSPSLXELIONSFVLVSASL--KISR--ASSKEHCSS

MHEALHNTYOKSLSLSPGK
 LH-----SLSRERGRSSSNVALARRRCRTPMASSWYTKTLXGPGFGMGSRVSPPEALATPPAPAR
 630 640 650 660 670 680 690
 XSPSRORSILPAMETMKSLOS
 700 710

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-617-619-8.res made by jdelaval on Tue 15 Feb 105 11:34:34 PST.

Query sequence being compared: US-10-617-619-8 (1-641)

Number of sequences searched: 6

Number of scores above cutoff: 6

Results of the initial comparison of US-10-617-619-8 (1-641) with:
File : trans.pep

100-
N -
U 50-
M -
B -
E -
R -
O -
F 10-
S -
E 5*
O -
U -
E -
N -
C -
B -
S 0-
SCORE 0 71 142 213 284 354 425 496 567 638
STDV 1 1 1 1 1 1 1 1 1 1

PARAMETERS

Similarity matrix Unitary K-tuple
Mismatch penalty 1 Joining penalty 2
Gap penalty 1.00 Window size 20
Gap size penalty 0.05
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
113 9 257.12
Times: CPU
00:00:00.00 Total Elapsed
00:00:00.00

Number of residues: 4270
Number of sequences searched: 6
Number of scores above cutoff: 6

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Score	Std. Frame
1. US-10-030-203-12	Sequence 12, Application US/10030203	712	638	2.04	0
2. US-10-030-203-12	Sequence 12, Application US/10030203	712	638	2.04	0
3. US-10-030-203-12	Sequence 12, Application US/10030203	712	638	2.04	0
4. US-10-030-203-12	Sequence 12, Application US/10030203	712	638	2.04	0
5. US-10-030-203-12	Sequence 12, Application US/10030203	712	638	2.04	0
6. US-10-030-203-12	Sequence 12, Application US/10030203	712	638	2.04	0

1. US-10-617-619-8 (1-641)

US-10-030-203-12 Sequence 12, Application US/10030203

Sequence 12, Application US/10030203
GENERAL INFORMATION:
APPLICANT: Alan Garten
APPLICANT: Zhiwei Hu
TITLE OF INVENTION: Neovascular-Targeted Immunoconjugates
FILE REFERENCE: OCR-679B US
CURRENT APPLICATION NUMBER: US/10/030,203
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: PCT/US00/16481
NUMBER OF SEQ ID NOS: 12
SOFTWARE: MS DOS
SEQ ID NO 12
LENGTH: 2138
TYPE: DNA
ORGANISM: Artificial Sequence
NAME/KEY: CDS
OTHER INFORMATION: hFv1asm immunoconjugate
OTHER INFORMATION: Includes leader + hFv1asm + human IgG1Fc

Initial Score = 638 Optimized Score = 638 Significance = 2.04
Residue Identity = 974 Matches = 628 Mismatches = 13
Gaps = 0 Conservative Substitutions = 0

KLCDPIVWSQALRLCLLGLGGLAAGVAKASGERTDMPKPPHRYVYQEAHGYLHRRBRANAFLL
10 20 30 40 50 60 70
XXLRPGSLRXCKKXKCSFXXARXIFPKDAXRTKLFWISYSDGDCASSPCQNGSCKDQLOSYICFLPAPF
BELRPGSLERCKEBCSFEARARIFPDABRTKLFWISYSDGDCASSPCQNGSCKDQLOSYICFLPAPF
80 90 100 110 120 130 140
GRNCETHKDOLICVNEGSCGEOYCSDHITGRKSCRCHEGYSILADGVSCTPYEYPCGKIPLEKRNASKP
GRNCETHKDOLICVNEGSCGEOYCSDHITGRKSCRCHEGYSILADGVSCTPYEYPCGKIPLEKRNASKP
150 160 170 180 190 200 210
OGRIVGKVCCKGSCPMQVLLVNGAOLCGSTLINTIYVWVAARCFDRIKWRNLIIVLGHDLSEHGDDEQ
OGRIVGKVCCKGSCPMQVLLVNGAOLCGSTLINTIYVWVAARCFDRIKWRNLIIVLGHDLSEHGDDEQ
220 230 240 250 260 270 280
SRRVAQVILPSTYVPGTTHDIALRLHQPVLVLDHVPVLCPLPRTSERTIARVRFELVSGMGLDORGAT
SRRVAQVILPSTYVPGTTHDIALRLHQPVLVLDHVPVLCPLPRTSERTIARVRFELVSGMGLDORGAT
290 300 310 320 330 340 350
ALELAVLVNVPRLMTQDCIQGSRKVDSPNITEVYFCAGYSDGSKDSCKDGSGPHATHYRGTWYLTLSVWG
ALELAVLVNVPRLMTQDCIQGSRKVDSPNITEVYFCAGYSDGSKDSCKDGSGPHATHYRGTWYLTLSVWG
360 370 380 390 400 410 420

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|||||
ALBELMTLVNRLMTQDLOOSRKVGSFNITETWFCAGYSGSKDSGAGSHAHYGTWLTITVWGM
370 380 390 400 410 420 430
OGCATYGHFVYTVRSQYIEMLOKMSBPRPGVLLRAPFGSABPKSCDTHTCPCPABELLGSGSVLFL
OGCATYGHFVYTVRSQYIEMLOKMSBPRPGVLLRAPFGSABPKSCDTHTCPCPABELLGSGSVLFL
440 450 460 470 480 490 500
PPRPKOTLMISRPPEVTCVVVDVSHEDPEVFENYVDGVEVNAKTKPRREQVSTYRVSVLTVLQDMLN
PPRPKOTLMISRPPEVTCVVVDVSHEDPEVFENYVDGVEVNAKTKPRREQVSTYRVSVLTVLQDMLN
510 520 530 540 550 560 570
GKEYCKVSNKALPAPRIEKTISKAKGQPRFQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQP
GKEYCKVSNKALPAPRIEKTISKAKGQPRFQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQP
580 590 600 610 620 630 640
ENNYKTPPVLDSGSEFLLYSKLTVDKSRMVOGQNVFSCSVNHEALHNYTQKSLSPGKX
ENNYKTPPVLDSGSEFLLYSKLTVDKSRMVOGQNVFSCSVNHEALHNYTQKSLSPGKX
650 660 670 680 690 700 710

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2. US-10-617-619-8 (1-641)

US-10-030-203-12

Initial Score = 11 Optimized Score = 60 Significance = -0.40
 Residue Identity = 17% Matches = 77 Mismatches = 299
 Gaps = 72 Conservative Substitutions = 0

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ANAFLLXLRGSLKRXCKXQCSFXHAKXIFKDAKXRTKLFWISDDQCSAPSCQNGSGCKDLOSYICPC
80 90 100 110 120 130 140
LPAFEGNETHKXDOQLCVNENGCCEQYSCDHTGTRSCRCHEGSLADGVSTPVEYPCGKIPILBKR
150 160 170 180 190 200 210
NAKPRQRIYGVKVCPCGECRQVYLLVNGAQLCGTLINTIYVNSAACHCDKIKAMRNILAVIGBIDLSBH
220 230 240 250 260 270 280
DGDEQSRRAQVILPSTYVPGTTHDIALRLHQPVVLTHTVPLCLPRTFSERTLA--FVRFSLVSGWQ
RPLIIVETGRSGSACSGCAEP--HASSMRBRSPATCGCPRAACCGRRSRS----
X 10 20 30 40 50
290 300 310 320 330 340 350
LIDRGA----TALBLMTLVNRLMTQDLOOSRKVGSFNITETWFCAGYSGSKDSGAGSHAHYGTWLTITVWGM
360 370 380 390 400 410
TWYLTG-----IVSMGCGCATVGHFG--VYTVRSQYIEMLOKMSBPRPGVLLRAPFGSABPK
WGLGGLCWRPCTCTPCGHSASPGAGRGXPHGFCCTAPRALSWYAPR--RPRSTXTPQGLRSGSRPP
130 140 150 160 170 180 190
420 430 440 450 460 470 480
SCDTHTCPCPABELLGSGSVLFLPPRPKOTLMISRPPEVTCVVVDVSHEDPEVFENYVDGVEVNAKTK-
RQKPRQSGRSGCQWVLGGGRLTVPRGVOVLGTVMGCBFCHKIWALRIRRMGLAGGLTALSAAXAPATR
200 210 220 230 240 250 260
-----KPRREQVSTYRVSVLTVLQDMLNKKEYCKVSNKALPAPRIEKTISKAKGQPRFQVYTL
490 500 510 520 530 540

```

3. US-10-617-619-8 (1-641)

US-10-030-203-12

Initial Score = 8 Optimized Score = 39 Significance = -0.41
 Residue Identity = 21% Matches = 53 Mismatches = 149
 Gaps = 50 Conservative Substitutions = 0

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GSDADITVRAVLLRLPRLCLGKNHLAIVHVPVELDLRVFAVHNNHACDLRGDHEGLGFMGEEDXRSP
150 160 170 180 190 200 210
OERCMARMACVSFVTRFGICSGSKNGSQEDSWAMLXANHLDPRLDVLGDPGVNPKRAHGCALAPADARQ
220 230 240 250 260 270 280
VPRAPVVGMMASTVPRAGVLAIRVAGTEHVLRIWGVSHLPLXLAVALGHOPGVHNNHLOGRGATVOQL
290 300 310 320 330 340 350
APAADCEVNEHGOPLREPRFGABEGHNVSEBHGVLQAEQRVVVVGAGADVDVAGDDDLBHPRLALPVVLA
370 380 390 400 410 420
EVLVLAQRDOVPPVLDVETVGRGHPDQGVDOGPPYQLSIIHQODLPWTLPRGAHLAP--HNSALDFAGIS
440 450 460 470 480 490 500
FXAXR-----XIF-----KDAKXRTKLFWISYSDG--DQCASSPCONGSGCKDLOSYICFCILPAFEGNRC
510 520 530 540 550 560 570
FPAKRRPSTWIFNCGCAGHPVCCQRPVLAIPALCARVYVTLAIVLVHNDOLVYIIVRLTVPALEGREBA
580 590 600 610 620 630 640
ETHKDDQL-----ICVNEGGEQECSDHTGTRSCRCHEGSLADGVSTPVEYPCGKIPIL--EKRN
650 660 670 680 690 700 710
BADIGELVLAGAPILAWTYGTVPITVTRNPEODLRLRVLEJDLPGLLBG--ALLLLALPLOGAARPOLDERVG
150 160 170 180 190 200 210

```

ASRQGRIVG-----GKVCRCSCPMQVLLVNGAQLCGSTLINTIIVVSAACFDKIKMWNLIIVLAGEH
 APAPVQAVGFLLEDYDVSVP--RLPRHV-----PCFSSXGLSDPACQALKPKQK-----ABEP-
 650 660 670 680 690 700
 220 X 230 240 250 260 270 280
 DLSHDDDSRRVAQVILPSTVYVPGTTNHDIALRLHQPVVLTQVPLCLPRTSERETIAFVRPSLVSG
 --GLGDHDEISA⁷¹⁰
 290 300 310 320 330 340 350
 MGQLLRGATALBLAMVNLVRLMTQDCLQGRKVDSPNITEYMFCAGYSDGSKDSCGSGPHATHYRGT
 360 370 380 390 400 410 420
 WYLTGIYVSGQGCATVGHFVYTVVSVQVIEWLOKLMRSEPRPVILARFPGSABRPSCDKTHTCPCPPABE
 430 440 450 460 470 480 490
 LLGGPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVNAKTKPREEQYNSTYRVVSV
 500 510 520 530 540 550 560 570
 LITLHQMVLNGSKTKCKVSKNKAIPARIKTISSKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFIPPSDI
 580 590 600 610 620 630 640
 AVEMESNGQPENNYKTPPVLDSDGSFELYSKLTVDKSRMQQGNVFCSCVMEALHNHYTQKSLSLSPGK

4. US-10-617-619-8 (1-641)
 US-10-030-203-12

Initial Score = 8 Optimized Score = 57 Significance = -0.41
 Residue Identity = 21% Matches = 81 Mismatches = 222
 Gaps = 67 Conservative Substitutions = 0

AAAYHLPGDBERLECVWMLCRASCITHEKTPCCCHLLSTVSLLRKQESBSGSGVILXLPSCGPLLSH
 10 20 30 40 50 60 70
 STAMSLGXKULTRQVRLTWFLVSSRRDGRVYTCXSRGCPALAMVPSMGARLLLETLLHYSLPFSQSWCR
 80 90 100 110 120 130 140
 TVRLTLTRVYLLYCSRSGLFYLAKCTSPSTYQMLNLTGSSWLTSTTTHVTSVGEIEMKRSVLGFGKRTQDP
 150 160 170 180 190 200 210
 PRSSGAGHGHHVYVLSQDLSADRGNGABRRTPGRGSRMSFCSSHMYMTLTYTPKMTVAQMPQUTMPV
 220 230 240 250 260 270 280
 RYHVPRXWVACGPPLSPAQESLPRSEXPAQNMYSVIFGESPTFRDCCRQSWIVISRGTLSTNSRPAVAPRSS
 290 300 310 320 330 340 350 360
 X ANAFLXLRPGLSLRXCKXKXCSFKXAKIIFQDAKTKLFWISYSNG-DQCA-----SSP
 370 X 380 390 400 410 420
 WPOPLTEKRTKSLVLENNVSG-ROGRTWSVRTGWC--RSSAMSWLVPGTYVLGMWTCATRLCSP
 430 440 450 460 470 480
 CQNGSGC--KQOLSYICFLPARBGRNCEHKKDQILCVNENGCEQYCSGDTGTSKSCCHSYSL
 490 500 510 520 530 540 550
 SCSLRSCSPSTAIRFLPLILSKQMAAE-----TQWVILIRV-----PHNXPAPFTNNTC--HGHSP
 560 570 580 590 600 610
 ADGVSTPTTYEYRPGKRIIEKRNASKPQG-RIVGKVCY--KQBCP--QVIL-LVNGAQLC-----GGT
 620 630 640 650 660 670 680 690 700
 --GHTLEPT-IRPWGLAPLFSRIGIRPHGYSTVGQDTPSASRBYPSMHOBLVPMWSLQYCSQPPSPFT
 710 720 730 740 750 760 770 780 790 800
 LINTIIVVSAACFDKIKMWNLIIVLAGEHLSF---HDEGDSRRVAQVILPSTVYVPGTTNHDIAL--R
 810 820 830 840 850 860 870 880 890 900
 OI--SNWSLVCVSGRPSKAGKQIXDWSWSLQPPFWHGLE-----AHWSPLKXIONSFPVLASASIKISR
 910 920 930 940 950 960 970 980 990 1000

250 260 270 280 290 300 310
 LHQVVLTDVHVPCLPERFSEETLLA---FVRFSLVSGN-GQLLDRGATALBLAMVNLVRLMTQDCLQ--
 ASSRHCSSLSLSRERGRSSSNALARRRCRTPMASWVTYTLXLPFGFGMSRVBPRLATPPARAPRX
 620 630 640 650 660 670 680 690
 320 X 330 340 350 360 370 380
 --SRKVDSPNITEYMFCAGYSDGSKDSCGSGPHATHYRGTWYLTGIYVSGQCATVGHFVYTVVSVQY
 SPGR-RORSLRAMEWTKLSQ
 700 710 X
 390 400 410 420 430 440 450
 IEWLOKMRSEPRPVILARFPGSABRPSKCDKTHTCPCPABELLGGPSVFLPPPKKDTLMISRTPEVTC
 460 470 480 490 500 510 520
 VVVDVSHEDPEVKFNMYVDGVEVNAKTKPREEQYNSTYRVVSVLITLHQMVLNGSKTKCKVSKNKAIPARIE
 530 540 550 560 570 580 590
 KTISSKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFIPPSDIAVEMESNGQPENNYKTPPVLDSDGSF
 600 610 620 630 640
 LYSKLTVDKSRMQQGNVFCSCVMEALHNHYTQKSLSLSPGK

5. US-10-617-619-8 (1-641)
 US-10-030-203-12

Initial Score = 7 Optimized Score = 98 Significance = -0.41
 Residue Identity = 19% Matches = 139 Mismatches = 418
 Gaps = 143 Conservative Substitutions = 0

ALQRTFHGLGCPQAPLPASASLPGCRBRGXLRNRTGHAIVAGASQSLRNCGSPRRAPAPARQVVC
 10 20 30 40 50 60 70
 X ANAFL-----XXLR--PQSL-XRCKXKXQCSF--XXAXIIFQDAKTKLFWISYSDGQCAASPCQN
 80 90 100 110 120 130 140
 GAAAGLPGEGVGGANVLIRGGPFGDLQGRGEVAVLDFLOXWGPCLKSMEMGL-LGGAPVLYLILPPCLR
 150 160 170 180 190 200
 GSGKQDLOQSYICFLPARBGRNCEHKKDQILCV-NENGCEQYCSGDTGTSKSCR-----CHEGSLD
 210 220 230 240 250 260 270
 GPBLXD-----AQGAPR---DLCE--REBRLXAVLOXPHGHQALLSVPRGVLSAGRGVLTHTSXISMKN
 280 290 300 310 320 330 340
 GVS-----CTPTVEYRPGKRIIEKRNASKPQGRIVGKVCYCPKQBCPMQVIL--LVNGAQLCGSTLINTIIVV
 350 360 370 380 390 400
 TYSRKKKCCQQTTPRNCG-GQGVFORGVS-MAGPYVGSWSVVMQDPLQHHILGGLRGFLFRONQELBEPDRCA
 410 420 430 440 450 460
 190 200 210 220 230 240 250
 SAACHPDKIXMWNLIIVLAGEHLSHDEGDSRRVAQVILP-----STVYVPGTTNHDIAL--
 260 270 280 290 300 310 320 330 340
 GRAPQARRGKXABPAGAGAHHPQHVPRGHQPRHAPAPAPARPGPHKPCGAPLPARTVLXEDAGRALIL
 350 360 370 380 390 400
 --LHQVVLTDVHVPCLPERFSEETLLA-FVRFSLVSGN-GQLLDRGATALBLAMVNLVRLMTQDCLQ--
 410 420 430 440 450 460
 GQRL-----GPAAGWRHGGPGAHGQARAPADDPG---LPAVT--EGGRLEKTHGAVLCCILGQ
 470 480 490 500 510 520
 OSRKVDSPNITEYMFCAGYSDGSKDSCGSGPHATHYRGTWYLTGIYVSGQCATVGHFVYTVVSVQY
 530 540 550 560 570 580 590 600
 QGLIRGQMRPT-----CHPLRGHVVDGHRQLGP-GLRNNG--PLNG-VHOGLPVIRVAAKAAHALATPRS
 610 620 630 640 650 660 670 680 690 700

```

-----QYIEMLOKMBRSPRGVTLARPPGASBPSCDKHTCP---PCPABELLGSPVFLPPKPKDT
470 480 490 500 510 520 530
PRASPTSRIRRAIILQNSHMPVSTXTPGGVSLPLPPKIQGHFDLPDGHMRGG--GREPRRXGQVQ
450 460 470 480 490 500 510
LMISRPETTC---VVVDVSHDEPKFMYVDGVVNAKTKPREBOYNSYTRVSVTLVHODMLNKE
LVGRGRGAXCCODKAGAAVQCHVP-----CGGRPHRAPGLAEWQ-----GVQV-OGIQQSPSPHR
540 550 560 570 580 590
520 530 540 550 560 570
YKCKNSNKA-----LPAPIETKISKAGQPREPOVYTL-----PPSRDELTKNOVSLTCLVKGFF
ENHLOSGRARPRTTGVHPAPVIFPGXADQBPQDPLPGQRLISQHRKRGVGEQMAAGELQDHASRAGIRLL
600 610 620 630 640 650 660
570 580 590 600 610 620 630
PBDIAVEMESNGQPENNYKTPPVTL-DSQSPFLYSKLTVDKSRMOQGNVFCSSVHMEALHNHYTQKSLSL
PLQQA---HRGQEQVAAGBRLLMLRDAGS---AOPLAHEEPLVPSGXNIG
670 680 690 700 710
640
PGK

```

6. US-10-617-619-8 (1-641)
US-10-030-203-12

Initial Score = 7 Optimized Score = 42 Significance = -0.41
Residue Identity = 19% Matches = 62 Mismatches = 187
Gaps = 70 Conservative Substitutions = 0

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SFAEISWGPSPSGSAFCIGFRAAVLQAGSLRPOEBKHGTCSRLTSSKXPRRKPTASCTGAGAPTRSW
10 20 30 40 50 60 70
RSCGRAPWFGASARRSAPSRPRGSSRRTRGRSCGFLVTWGTSPQVHARMGAPARTSSPISASASLPSR
80 90 100 110 120 130 140
ACTVRRTRMTSXSVXTRTAVASSTAATVTRAPASVATRGTLCMOTGCPAHPOLNITVEKYLFXKKEMPANP
150 160 170 180 190 200 210
KAEIAGARCAPKGSVHGRSCCMXMEISCVGGKSTPSGMSPPRTVSTKSTFGTIXSRCAWASTTSASTGMSR
220 230 240 250 260 270 280
AGGWRSSSPARTSRAPPTTTSRCSACTSPWSLTMCPGACPNGRSLRGMWPSCASHWGAGASCTVAPR
290 300 310 320 330 340 350 360
PWSMWCSTPGKXPRTAGSGHGRWETPOISRSTCSVPATMAARTPARGTVEAHMPPTTGAGGTXRASAGA
370 380 390 400 410 420 430
X' 1D 20 30 40 50
ANAPLXLAPG--SLXRXCKXQCSFXXA-----RXIFPD-----AXRTKLFMISYSDGDCASSPCQN
440 450 460 470 480 490
RAAQWATL-GCTPGSPSTSSGCK-SSCAQSHAQESSCEPHFPDPQSPNIVTL---THAARAQHLANSWGDR
60 70 80 90 100 110 120
GGSCKDQ-LQSYICFLPAFEGNRCETHDODLICVNEGSGEQYCSDHNGTKRSRC-----HEGYS--LLA
130 140 150 160 170 180
QSSSSQNPRTPSXSPGPIRSHAMWMTXATKTL-----RSSSTGTWTAMCIXPRQSRGSSTTA
190 200 210 220 230 240 250
DGV-----SCTPTVEYPCGKIPILKRNASKPGQRIYGGKVCPEQWQVLLVNGAQLCGTILINTIIV
260 270 280 290 300 310 320
RTVMASASSPSCRTT-GXMAKSTASAPTPPSQPPSKRPSK--PKG---SPENXRCCTPCPHPMGMSXPRT---
330 340 350 360 370 380 390
190 200 210 220 230 240 250

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VSAHCFDKIKWNRNLIATVLSGHDLSHDG-DEOSRRVAQVILPSTYVPGTTHNDIA--LLRLHOPVLTIDH
260 270 280 290 X 300 310 320
RSXAPWMSK-----ASIPATSPMSGRAMGSRRTTRRLPCMTPTAPASSSTASSPWTAGSGRGTS
630 640 650 660 670 680
260 270 280 290 X 300 310 320
VVPCLPERTFSERTLAFVRFSLVSGWGLDRGATALMLVNLVPRMTQDCLQOSRKVGDSPNITBEVNC
HAPXCMRLCTTTTTRRA-----SPCLAVNDRP
690 700 710 X
330 340 350 360 370 380 390 400
AGYSDSKDSCKDGSGPHATYRGTWYLTGLIVSMQGCATVGHFGYTRVSGYIEMLOKMBRSPRGVTL
410 420 430 440 450 460 470
RAPFPGSABPKSCDKHTHTCPPCPAPBELDGPVFLFPKPKDTLMSRTPEVTGVVDVSHDEPKFMYV
480 490 500 510 520 530 540
DGYEVHNAKTKPREEQYNSTYRVSVTLVHODMLNGEKYCKVSNKALPAPIETKISKAGQPREPOVYTL
550 560 570 580 590 600 610
PPSRDELTKNOVSLTCLVKGFFPSDIAVEMESNGQPENNYKTPPVTLDSQSPFLYSKLTVDKSRMOQGNV
620 630 640
SCSVMEALHNHYTQKSLSLSPGK

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